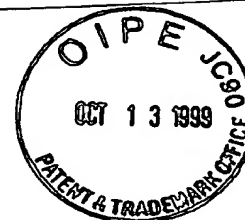


SEQUENCE LISTING



<110> HOLMGREN, Lars
TROYANOVSKY, Boris

<120> Angiogenesis Related Molecules

<130> 3362-101P

<140>

<141>

<150> 60/114,386

<151> 1998-12-29

<150> 60/089,266

<151> 1998-06-15

<150> SE9804372-2

<151> 1998-12-17

<160> 15

<170> PatentIn Ver. 2.1

<210> 1

<211> 6463

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (797) .. (2824)

<400> 1

ccaggagctg ccttggcagt cacgcccctt ccttccgagg agctttcttg ctgcctaaac 60
tggtagaccc cctgaattac tctccatct ccgctctctt tcgcctctc ttctcttagt 120
tctctccgcc tccccctcaa ctaccaccac ctccagtcag tctgcctcc ggctatccgc 180
tgctccaccc tctggcccggt tatcctgcct gtccgctgcc accaaggaga gcccgagcgg 240
agcagcaggg aggggagcag ccgggagttg gggcttcccc cctgcccata cctggccgct 300
ggcccgggac cgaagccact tgagcgagca gagatcgct accttgtctt ctttgccttc 360
agggagctgc taagaaggac aaataagata gcagagtga agagcttttg tctccttaga 420
aggaaggctg agaaactaaa ggccagcgca ggacatctca ttgccattgt cagccaggaa 480
ctcgcagcct cacagcccta cttcttctct gacctctggg gggctccttg ccttgctaca 540
atctccacca tccactagat tgtctcctgc ccgacacccc ttgggtccaa accagggaga 600
ccattcagct cacctgccta ggccgcagca gcatttcctt cctaatacagg ctaccaggg 660
ggatcattac cgtctctccc aacctggcct gagtcagcag cagcagcaac agcagcagca 720
gcaccatcat caccatcacc accaacaaca gcagcagcag cagccacagc agcagccagg 780

agaagcctat tcagct atg cct cgg gct cag cca tcc tct gct tct tat cag 832
Met Pro Arg Ala Gln Pro Ser Ser Ala Ser Tyr Gln
1 5 10

cca gtg cca gca gac cct ttt gcc att gtt tcc aga gcc cag cag atg 880
Pro Val Pro Ala Asp Pro Phe Ala Ile Val Ser Arg Ala Gln Gln Met
15 20 25

gtt gag atc ctc tca gac gag aac cgg aac ttg agg caa gag ttg gaa 928
Val Glu Ile Leu Ser Asp Glu Asn Arg Asn Leu Arg Gln Glu Leu Glu
30 35 40

gga tgc tat gag aag gtg gca aga ctg cag aag gtg gag aca gaa atc 976
Gly Cys Tyr Glu Lys Val Ala Arg Leu Gln Lys Val Glu Thr Glu Ile
45 50 55 60

cag cgc gtc tcg gag gca tat gag aac ctc gtg aag tca tcc tcc aaa 1024
Gln Arg Val Ser Glu Ala Tyr Glu Asn Leu Val Lys Ser Ser Ser Lys
65 70 75

aga gag gcc cta gag aaa gcc atg aga aac aag cta gag ggc gag att 1072
Arg Glu Ala Leu Glu Lys Ala Met Arg Asn Lys Leu Glu Gly Glu Ile
80 85 90

cgg agg atg cat gat ttc aac agg gat ctg aga gag cgt cta gag act 1120
Arg Arg Met His Asp Phe Asn Arg Asp Leu Arg Glu Arg Leu Glu Thr
95 100 105

gcc aac aag cag ctt gca gag aag gaa tat gag ggg tca gag gac acc 1168
Ala Asn Lys Gln Leu Ala Glu Lys Glu Tyr Glu Gly Ser Glu Asp Thr
110 115 120

aga aaa acc atc tcg cag ctc ttt gca aaa aat aaa gaa agc cag cgt 1216
Arg Lys Thr Ile Ser Gln Leu Phe Ala Lys Asn Lys Glu Ser Gln Arg
125 130 135 140

gag aag gag aag ctg gaa gcg gag ctg gcc act gcc cgt tct acc aat 1264
Glu Lys Glu Lys Leu Glu Ala Glu Leu Ala Thr Ala Arg Ser Thr Asn
145 150 155

gag gac caa aga cga cac atc gaa atc cga gat cag gcc ctg agt aat 1312
Glu Asp Gln Arg Arg His Ile Glu Ile Arg Asp Gln Ala Leu Ser Asn
160 165 170

gcc cag gcc aag gtg gta aag ctg gaa gaa gag ctg aaa aag aag caa 1360
Ala Gln Ala Lys Val Val Lys Leu Glu Glu Glu Leu Lys Lys Lys Gln
175 180 185

gtg tac gtt gac aag gtg gag aag atg cag cag gcc ctt gta cag ctc 1408
Val Tyr Val Asp Lys Val Glu Lys Met Gln Gln Ala Leu Val Gln Leu
190 195 200

cag gca gca tgt gaa aaa cgt gag cag cta gag cac cgt ctc cgg aca 1456
Gln Ala Ala Cys Glu Lys Arg Glu Gln Leu Glu His Arg Leu Arg Thr
205 210 215 220

cga ctg gag agg gaa ctg gaa tcc ctg aga atc cag cag cgt cag ggc 1504
Arg Leu Glu Arg Glu Leu Glu Ser Leu Arg Ile Gln Gln Arg Gln Gly
225 230 235

aac tgt cag ccc acc aac gtt tca gaa tac aat gct gcc gca ctg atg 1552

Asn	Cys	Gln	Pro	Thr	Asn	Val	Ser	Glu	Tyr	Asn	Ala	Ala	Ala	Leu	Met	
			240					245						250		
gag	ctc	ctt	cgg	gag	aaa	gag	gag	agg	att	ctg	gct	ctg	gaa	gct	gat	1600
Glu	Leu	Leu	Arg	Glu	Lys	Glu	Glu	Arg	Ile	Leu	Ala	Leu	Glu	Ala	Asp	
		255					260					265				
atg	aca	aag	tgg	gag	cag	aaa	tat	ttg	gag	gag	aat	gtg	atg	aga	cat	1648
Met	Thr	Lys	Trp	Glu	Gln	Lys	Tyr	Leu	Glu	Glu	Asn	Val	Met	Arg	His	
	270					275					280					
ttt	gct	ctg	gat	gct	gct	gca	act	gtg	gct	gct	cag	agg	gac	aca	aca	1696
Phe	Ala	Leu	Asp	Ala	Ala	Ala	Thr	Val	Ala	Ala	Gln	Arg	Asp	Thr	Thr	
285					290					295					300	
gtc	atc	agt	cac	tct	cct	aac	acc	agc	tat	gac	aca	gct	cta	gaa	gct	1744
Val	Ile	Ser	His	Ser	Pro	Asn	Thr	Ser	Tyr	Asp	Thr	Ala	Leu	Glu	Ala	
			305						310					315		
cgc	atc	cag	aaa	gag	gag	gaa	gaa	atc	ttg	atg	gcc	aat	aag	cgt	tgc	1792
Arg	Ile	Gln	Lys	Glu	Glu	Glu	Glu	Ile	Leu	Met	Ala	Asn	Lys	Arg	Cys	
			320					325					330			
ctt	gac	atg	gag	ggc	agg	att	aag	acc	ctc	cat	gcc	cag	att	att	gag	1840
Leu	Asp	Met	Glu	Gly	Arg	Ile	Lys	Thr	Leu	His	Ala	Gln	Ile	Ile	Glu	
		335					340					345				
aag	gat	gcc	atg	atc	aaa	gta	ctc	cag	cag	cgt	tcc	cgg	aag	gag	ccg	1888
Lys	Asp	Ala	Met	Ile	Lys	Val	Leu	Gln	Gln	Arg	Ser	Arg	Lys	Glu	Pro	
	350					355					360					
agc	aag	aca	gag	cag	ctg	tcg	tgc	atg	cgg	cca	gcg	aag	tct	ctg	atg	1936
Ser	Lys	Thr	Glu	Gln	Leu	Ser	Cys	Met	Arg	Pro	Ala	Lys	Ser	Leu	Met	
365					370					375					380	
tcc	att	tcc	aat	gct	gga	tca	ggc	ttg	ctc	tcc	cac	tca	tcc	acc	ctg	1984
Ser	Ile	Ser	Asn	Ala	Gly	Ser	Gly	Leu	Leu	Ser	His	Ser	Ser	Thr	Leu	
			385					390						395		
act	ggc	tcc	ccc	atc	atg	gaa	gaa	aag	cga	gac	gac	aag	agc	tgg	aag	2032
Thr	Gly	Ser	Pro	Ile	Met	Glu	Glu	Lys	Arg	Asp	Asp	Lys	Ser	Trp	Lys	
			400					405					410			
ggg	agc	cta	ggc	att	ctc	ctg	ggt	gga	gac	tac	cgt	gct	gaa	tat	gtc	2080
Gly	Ser	Leu	Gly	Ile	Leu	Leu	Gly	Gly	Asp	Tyr	Arg	Ala	Glu	Tyr	Val	
		415					420					425				
cct	tcc	aca	ccc	tcg	cct	gtg	cca	ccc	tcg	act	ccc	ctg	ctc	tcg	gct	2128
Pro	Ser	Thr	Pro	Ser	Pro	Val	Pro	Pro	Ser	Thr	Pro	Leu	Leu	Ser	Ala	
		430				435					440					
cac	tcc	aag	aca	ggc	agc	cga	gac	tgc	agt	acc	caa	act	gaa	cgt	ggg	2176
His	Ser	Lys	Thr	Gly	Ser	Arg	Asp	Cys	Ser	Thr	Gln	Thr	Glu	Arg	Gly	
445					450					455					460	
acg	gaa	tcg	aac	aaa	act	gca	gct	gtt	gct	ccc	atc	tct	gtt	cct	gct	2224
Thr	Glu	Ser	Asn	Lys	Thr	Ala	Ala	Val	Ala	Pro	Ile	Ser	Val	Pro	Ala	
			465					470						475		
cca	gtt	gct	gct	gcc	gcc	act	gct	gcc	gcc	atc	act	gcc	act	gct	gcc	2272
Pro	Val	Ala	Ala	Ala	Ala	Thr	Ala	Ala	Ala	Ile	Thr	Ala	Thr	Ala	Ala	

480										485										490										
acc	atc	acc	acc	acc	atg	gta	gct	gct	gct	cca	gtt	gct	gtt	gct	gct	2320														
Thr	Ile	Thr	Thr	Thr	Met	Val	Ala	Ala	Ala	Pro	Val	Ala	Val	Ala	Ala															
495					500					505																				
gct	gct	gct	cca	gct	gct	gct	gct	gcc	ccg	tct	cca	gcc	act	gcc	gct	2368														
Ala	Ala	Ala	Pro	Ala	Ala	Ala	Ala	Ala	Pro	Ser	Pro	Ala	Thr	Ala	Ala															
510			515			520																								
gct	act	gct	gct	gct	gtt	tct	cca	gct	gct	gct	ggg	cag	att	cca	gct	2416														
Ala	Thr	Ala	Ala	Ala	Val	Ser	Pro	Ala	Ala	Ala	Gly	Gln	Ile	Pro	Ala															
525		530		535		540																								
gct	gcc	tct	gtt	gcc	tca	gct	gct	gcc	gtt	gct	cct	tct	gct	gct	gct	2464														
Ala	Ala	Ser	Val	Ala	Ser	Ala	Ala	Ala	Val	Ala	Pro	Ser	Ala	Ala	Ala															
545				550				555																						
gct	gct	gct	gtt	cag	gtt	gct	cca	gct	gct	ccg	gct	cca	gtt	cca	gct	2512														
Ala	Ala	Ala	Val	Gln	Val	Ala	Pro	Ala	Ala	Pro	Ala	Pro	Val	Pro	Ala															
560			565			570																								
ccg	gct	ctg	gtt	ccg	gtt	cca	gct	cca	gca	gcg	gct	cag	gct	tct	gct	2560														
Pro	Ala	Leu	Val	Pro	Val	Pro	Ala	Pro	Ala	Ala	Ala	Gln	Ala	Ser	Ala															
575		580		585																										
cct	gct	cag	act	cag	gca	cca	act	tca	gct	ccg	gct	gtg	gct	cca	act	2608														
Pro	Ala	Gln	Thr	Gln	Ala	Pro	Thr	Ser	Ala	Pro	Ala	Val	Ala	Pro	Thr															
590		595		600																										
cca	gct	cca	act	cca	act	cca	gct	gtg	gct	cag	gct	gag	gtt	cct	gca	2656														
Pro	Ala	Pro	Thr	Pro	Thr	Pro	Ala	Val	Ala	Gln	Ala	Glu	Val	Pro	Ala															
605		610		615		620																								
agt	cca	gct	acc	ggg	cct	gga	cca	cat	cgt	ttg	tct	ata	cca	agt	ttg	2704														
Ser	Pro	Ala	Thr	Gly	Pro	Gly	Pro	His	Arg	Leu	Ser	Ile	Pro	Ser	Leu															
625			630			635																								
acc	tgc	aat	cca	gac	aaa	aca	gat	ggg	cct	gtg	ttc	cac	tcc	aat	act	2752														
Thr	Cys	Asn	Pro	Asp	Lys	Thr	Asp	Gly	Pro	Val	Phe	His	Ser	Asn	Thr															
640			645			650																								
ctg	gaa	aga	aaa	act	ccc	att	cag	atc	ctg	gga	caa	gag	cct	gat	gca	2800														
Leu	Glu	Arg	Lys	Thr	Pro	Ile	Gln	Ile	Leu	Gly	Gln	Glu	Pro	Asp	Ala															
655		660		665																										
gag	atg	gtg	gaa	tat	ctc	atc	taa	acggccaaat	caagagctgc	agattatcag	2854																			
Glu	Met	Val	Glu	Tyr	Leu	Ile																								
670		675																												
caaaaatgct tttaatcatt ttcccccttt tattggttct tgttttgagg gtgaggacaa 2914																														
gggttggtggg gaggggatgt tttttaacag gactttttat tggaacaatg tactacttga 2974																														
gtaataccat gtgaacacca gtctattttg gtatgcttag ggagtacctc taaagacaga 3034																														
ttaatcagaa tgtgctctaa agcttattgt ttgaatttat acgaatactg ggactgttaa 3094																														
caggtggcta tacatcgacg ttttcaatgt gcttaaattt gtttaaattt tccatattct 3154																														
agatcatttt ttattgaaga gcacagtatg tgtggaagac agtgtataac acgtagtttg 3214																														

gaagtgggaa gctagagaga attgagtgtg tgctgttttg tatagttact atcctgtgca 3274
 gcagctggag aaagcactca cctcaggctt acaaaaggga atagtttcag gagctatgta 3334
 agctggaaaa aaggtagga gttttggggt gcagaagggt actggagcta attttttctt 3394
 ccagtttccc agctaccctg cccagggaa ttgtgtttgt cttcatttca gtggtgcttt 3454
 ggaaatggat tcttttggtt cctcctgga ggttcataca ttcatatata tgctctggag 3514
 taatttatgc atttgataa ttaatatatt gctttcagat gctgggagag tacattaact 3574
 gagtgatgcg caacttctc tctcttaggg aattagacca tcagaggcct tgatggagag 3634
 ttgcatgggg tgctatatgc agacttccat ggtttgtgtg tagccatgaa cacagcttgc 3694
 ttgcatttag taagaccaat cagcttagtg tttatttctt ctacagcaca gattcactgg 3754
 ctgggtctcc agtctcaa at tgccaatcat ttgcaaagt aggaaggatc tttgttgaca 3814
 gggtgaatgc tttgaatttc tgggtgactac tttgaaataa cttgttttgt ttgtcaaatt 3874
 ctaagcatat gtcttaaaag gcatttttga ctatcacctc caaggaata gcttgagaaa 3934
 cccaaagtac tatgctgcag tcgggggaga ggtggattgc agcagtatcc tcaactacct 3994
 cttctcactg tcagtgcac catcttgga tacctttggg aagcagcagg aaatgtgcat 4054
 gtgggtagag atcaaaggag gcaatggctc caagccttgc catagggctg cctccaagga 4114
 cacagaagga tgccagttgc cacaggctcc tgcctgtgtg cacctgtctg cccttcatta 4174
 aggtgagaaa tctgcagata gcatcattaa gatcagtttt aaggggtata gggagggtga 4234
 gggaagtggg ggggtgtagg taagggttg gggtagaggt tttgggatgt cttagttaga 4294
 aaccagatta atagaagagt aggcctgata tattacatca tgagccatag tgggtgggaaa 4354
 gaacttttagc aatatagccc tacctcctca ttttagtgat gaggaatctg agaactggag 4414
 aggttcagtg actttttgaa agtcatacaa cacagctaac cattatgcca atcaccatgc 4474
 ttattttggg aaactcttta tcttttttaa attccatttt atgaaaaggc atcttcatgg 4534
 tccagggaat atgtatcttg taaaatgtac ctgggtggag tagcttgtcc agtcttgaca 4594
 aactactgaa tttctgtctt gcctctcctt cagtgccttt taaaagggtt tcccttttct 4654
 gatctgcatt tcaacataga gtcacataaa tgtccccctg agaaaccaat cccacttctt 4714
 tctaggagat tgggtatctt agataatctt ttgggggttcc tctgtgagta taggaatggg 4774
 atccttctta attatcttcc aaaggaatta ttttgtgtgt gtgcctgtgt gtgtgtagag 4834
 acataaagga gggatggtg attttcagct agtcctttca ctttttcaat aatgaggtaa 4894
 tcatgttaca tacacattag tcctcagtta taaagtgaat ctcagataga aattaaaagt 4954
 gcagttgtgt taagactctt tcatactacc ctttagtcat aaggagaaaa aaactcaaa 5014

atagtagaag cagcaagtag caaacttcag gagagctact ttctatccaa ataatttaaa 5074
 aaacactttt cacctactcc tttcatgggtt ataacacatt ggcagacttt ttgctggctc 5134
 tgggagccat gattttaate acattctgca aggtgacaaa tgtcatacat tccacattgt 5194
 gtggtagcca tctctttaga ctcatgtgtt ttggggaaaag gaagaagttc ttggctgagt 5254
 actattttga actttccaga accctctcac accagagaca gttcttctct gttcagtttc 5314
 caatccccga taatttgcta aaataacatt gtacatccaa gagagggaag aagagtatgt 5374
 cagtatatta tgcagaagat agatacagcc ttttcagaag atctccacta gtttttgttc 5434
 caaaaattca agtttatggg agaaatctca attagccacc ttttcacagt tgtgtggata 5494
 taacatttgg gggatcttcc tggactccta cctatctgtg cattttaccg gcacctcagg 5554
 aaaggagggt gaccagggtg tcttagcttg tactgcttgg tgatctctga ggaccttcta 5614
 attcagttgt accccagtgt tccatgtata gaaaaacttc attagaacaa actttacttg 5674
 atatgaaact cctattaaca gtcttttttt gaaataaaaa gtagcttgag ctttctttta 5734
 aatcatgta tcttgattgt tgatttaatg aaggatttcc ttttaatgct gcttttgagc 5794
 ttcaaggtaa taggacagca ggaacctaaa atatctgcca tcatctgcca taggaaagat 5854
 acccagagac ccatcatgtt ctctttttgt tgttacactg ttgggtgggt ataacaattg 5914
 gaaaatgaac aaactgattg attgtgcaaa ctacttttta tgacaagcct aaacctcat 5974
 aatgcggcag cttaaagtgt atacatatgc actaactttg atcaattata ttctcatatc 6034
 tgtagctac acagtctcct attatctcaa ttgcttatgt gcatatggaa tatgttactt 6094
 aaaacgtgtg cattcttact gaaaatgttt tcaaaggaag gtatcagctg tgggctaatt 6154
 gccaccaatt tcagcctgcc acgattcttg gaaatatgtc ttccaagtgc catccatcat 6214
 cagtaggaca agtgtcggga gtttgtttat tttttccag tagcaacgat gggttacatg 6274
 gagccatgaa acctccttct ggcctccctt gtgattaatg gcatgtgttt gtaaaatgga 6334
 tagctggggg tggcagatgg ctagagaaga atcgcttttg gtttaaaatg tatgtggtcc 6394
 cctaattgatt gtgaccccat tctgtaatca actgagctag ttccaataaa gttaagcagg 6454
 tttaaattcc 6463

<210> 2
 <211> 675
 <212> PRT
 <213> Homo sapiens

<400> 2
 Met Pro Arg Ala Gln Pro Ser Ser Ala Ser Tyr Gln Pro Val Pro Ala
 1 5 10 15

Asp Pro Phe Ala Ile Val Ser Arg Ala Gln Gln Met Val Glu Ile Leu
 20 25 30
 Ser Asp Glu Asn Arg Asn Leu Arg Gln Glu Leu Glu Gly Cys Tyr Glu
 35 40 45
 Lys Val Ala Arg Leu Gln Lys Val Glu Thr Glu Ile Gln Arg Val Ser
 50 55 60
 Glu Ala Tyr Glu Asn Leu Val Lys Ser Ser Ser Lys Arg Glu Ala Leu
 65 70 75 80
 Glu Lys Ala Met Arg Asn Lys Leu Glu Gly Glu Ile Arg Arg Met His
 85 90 95
 Asp Phe Asn Arg Asp Leu Arg Glu Arg Leu Glu Thr Ala Asn Lys Gln
 100 105 110
 Leu Ala Glu Lys Glu Tyr Glu Gly Ser Glu Asp Thr Arg Lys Thr Ile
 115 120 125
 Ser Gln Leu Phe Ala Lys Asn Lys Glu Ser Gln Arg Glu Lys Glu Lys
 130 135 140
 Leu Glu Ala Glu Leu Ala Thr Ala Arg Ser Thr Asn Glu Asp Gln Arg
 145 150 155 160
 Arg His Ile Glu Ile Arg Asp Gln Ala Leu Ser Asn Ala Gln Ala Lys
 165 170 175
 Val Val Lys Leu Glu Glu Glu Leu Lys Lys Lys Gln Val Tyr Val Asp
 180 185 190
 Lys Val Glu Lys Met Gln Gln Ala Leu Val Gln Leu Gln Ala Ala Cys
 195 200 205
 Glu Lys Arg Glu Gln Leu Glu His Arg Leu Arg Thr Arg Leu Glu Arg
 210 215 220
 Glu Leu Glu Ser Leu Arg Ile Gln Gln Arg Gln Gly Asn Cys Gln Pro
 225 230 235 240
 Thr Asn Val Ser Glu Tyr Asn Ala Ala Ala Leu Met Glu Leu Leu Arg
 245 250 255
 Glu Lys Glu Glu Arg Ile Leu Ala Leu Glu Ala Asp Met Thr Lys Trp
 260 265 270
 Glu Gln Lys Tyr Leu Glu Glu Asn Val Met Arg His Phe Ala Leu Asp
 275 280 285
 Ala Ala Ala Thr Val Ala Ala Gln Arg Asp Thr Thr Val Ile Ser His
 290 295 300
 Ser Pro Asn Thr Ser Tyr Asp Thr Ala Leu Glu Ala Arg Ile Gln Lys
 305 310 315 320
 Glu Glu Glu Glu Ile Leu Met Ala Asn Lys Arg Cys Leu Asp Met Glu
 325 330 335
 Gly Arg Ile Lys Thr Leu His Ala Gln Ile Ile Glu Lys Asp Ala Met

Tyr Leu Ile
675

<210> 3
<211> 675
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> () ..
<223> Residue 135 = Asn, Ser or Asp

<220>
<221> VARIANT
<222> () .. (150)
<223> Residues 148-150 = Glu-Leu-Ala or Thr-Thr-Pro

<400> 3
Met Pro Arg Ala Gln Pro Ser Ser Ala Ser Tyr Gln Pro Val Pro Ala
1 5 10 15
Asp Pro Phe Ala Ile Val Ser Arg Ala Gln Gln Met Val Glu Ile Leu
20 25 30
Ser Asp Glu Asn Arg Asn Leu Arg Gln Glu Leu Glu Gly Cys Tyr Glu
35 40 45
Lys Val Ala Arg Leu Gln Lys Val Glu Thr Glu Ile Gln Arg Val Ser
50 55 60
Glu Ala Tyr Glu Asn Leu Val Lys Ser Ser Ser Lys Arg Glu Ala Leu
65 70 75 80
Glu Lys Ala Met Arg Asn Lys Leu Glu Gly Glu Ile Arg Arg Met His
85 90 95
Asp Phe Asn Arg Asp Leu Arg Glu Arg Leu Glu Thr Ala Asn Lys Gln
100 105 110
Leu Ala Glu Lys Glu Tyr Glu Gly Ser Glu Asp Thr Arg Lys Thr Ile
115 120 125
Ser Gln Leu Phe Ala Lys Xaa Lys Glu Ser Gln Arg Glu Lys Glu Lys
130 135 140
Leu Glu Ala Xaa Xaa Xaa Thr Ala Arg Ser Thr Asn Glu Asp Gln Arg
145 150 155 160
Arg His Ile Glu Ile Arg Asp Gln Ala Leu Ser Asn Ala Gln Ala Lys
165 170 175
Val Val Lys Leu Glu Glu Glu Leu Lys Lys Lys Gln Val Tyr Val Asp
180 185 190
Lys Val Glu Lys Met Gln Gln Ala Leu Val Gln Leu Gln Ala Ala Cys
195 200 205
Glu Lys Arg Glu Gln Leu Glu His Arg Leu Arg Thr Arg Leu Glu Arg

210				215				220							
Glu	Leu	Glu	Ser	Leu	Arg	Ile	Gln	Gln	Arg	Gln	Gly	Asn	Cys	Gln	Pro
225					230					235					240
Thr	Asn	Val	Ser	Glu	Tyr	Asn	Ala	Ala	Ala	Leu	Met	Glu	Leu	Leu	Arg
				245					250					255	
Glu	Lys	Glu	Glu	Arg	Ile	Leu	Ala	Leu	Glu	Ala	Asp	Met	Thr	Lys	Trp
				260					265				270		
Glu	Gln	Lys	Tyr	Leu	Glu	Glu	Asn	Val	Met	Arg	His	Phe	Ala	Leu	Asp
		275					280						285		
Ala	Ala	Ala	Thr	Val	Ala	Ala	Gln	Arg	Asp	Thr	Thr	Val	Ile	Ser	His
		290				295					300				
Ser	Pro	Asn	Thr	Ser	Tyr	Asp	Thr	Ala	Leu	Glu	Ala	Arg	Ile	Gln	Lys
305					310					315					320
Glu	Glu	Glu	Glu	Ile	Leu	Met	Ala	Asn	Lys	Arg	Cys	Leu	Asp	Met	Glu
				325					330					335	
Gly	Arg	Ile	Lys	Thr	Leu	His	Ala	Gln	Ile	Ile	Glu	Lys	Asp	Ala	Met
			340						345				350		
Ile	Lys	Val	Leu	Gln	Gln	Arg	Ser	Arg	Lys	Glu	Pro	Ser	Lys	Thr	Glu
		355					360					365			
Gln	Leu	Ser	Cys	Met	Arg	Pro	Ala	Lys	Ser	Leu	Met	Ser	Ile	Ser	Asn
		370				375					380				
Ala	Gly	Ser	Gly	Leu	Leu	Ser	His	Ser	Ser	Thr	Leu	Thr	Gly	Ser	Pro
385					390					395					400
Ile	Met	Glu	Glu	Lys	Arg	Asp	Asp	Lys	Ser	Trp	Lys	Gly	Ser	Leu	Gly
				405					410					415	
Ile	Leu	Leu	Gly	Gly	Asp	Tyr	Arg	Ala	Glu	Tyr	Val	Pro	Ser	Thr	Pro
			420					425					430		
Ser	Pro	Val	Pro	Pro	Ser	Thr	Pro	Leu	Leu	Ser	Ala	His	Ser	Lys	Thr
		435					440					445			
Gly	Ser	Arg	Asp	Cys	Ser	Thr	Gln	Thr	Glu	Arg	Gly	Thr	Glu	Ser	Asn
		450				455					460				
Lys	Thr	Ala	Ala	Val	Ala	Pro	Ile	Ser	Val	Pro	Ala	Pro	Val	Ala	Ala
465					470					475					480
Ala	Ala	Thr	Ala	Ala	Ala	Ile	Thr	Ala	Thr	Ala	Ala	Thr	Ile	Thr	Thr
				485					490					495	
Thr	Met	Val	Ala	Ala	Ala	Pro	Val	Ala	Val	Ala	Ala	Ala	Ala	Ala	Pro
			500					505					510		
Ala	Ala	Ala	Ala	Ala	Pro	Ser	Pro	Ala	Thr	Ala	Ala	Ala	Thr	Ala	Ala
		515					520				525				
Ala	Val	Ser	Pro	Ala	Ala	Ala	Gly	Gln	Ile	Pro	Ala	Ala	Ala	Ser	Val
		530				535				540					

Ala Ser Ala Ala Ala Val Ala Pro Ser Ala Ala Ala Ala Ala Val
 545 550 555 560
 Gln Val Ala Pro Ala Ala Pro Ala Pro Val Pro Ala Pro Ala Leu Val
 565 570 575
 Pro Val Pro Ala Pro Ala Ala Ala Gln Ala Ser Ala Pro Ala Gln Thr
 580 585 590
 Gln Ala Pro Thr Ser Ala Pro Ala Val Ala Pro Thr Pro Ala Pro Thr
 595 600 605
 Pro Thr Pro Ala Val Ala Gln Ala Glu Val Pro Ala Ser Pro Ala Thr
 610 615 620
 Gly Pro Gly Pro His Arg Leu Ser Ile Pro Ser Leu Thr Cys Asn Pro
 625 630 635 640
 Asp Lys Thr Asp Gly Pro Val Phe His Ser Asn Thr Leu Glu Arg Lys
 645 650 655
 Thr Pro Ile Gln Ile Leu Gly Gln Glu Pro Asp Ala Glu Met Val Glu
 660 665 670
 Tyr Leu Ile
 675

<210> 4
 <211> 143
 <212> PRT
 <213> Homo sapiens

<400> 4
 Glu Ser Asn Lys Thr Ala Ala Val Ala Pro Ile Ser Val Pro Ala Pro
 1 5 10 15
 Val Ala Ala Ala Ala Thr Ala Ala Ala Ile Thr Ala Thr Ala Ala Thr
 20 25 30
 Ile Thr Thr Thr Met Val Ala Ala Ala Pro Val Ala Val Ala Ala Ala
 35 40 45
 Ala Ala Pro Ala Ala Ala Ala Ala Pro Ser Pro Ala Thr Ala Ala Ala
 50 55 60
 Thr Ala Ala Ala Val Ser Pro Ala Ala Ala Gly Gln Ile Pro Ala Ala
 65 70 75 80
 Ala Ser Val Ala Ser Ala Ala Ala Val Ala Pro Ser Ala Ala Ala Ala
 85 90 95
 Ala Ala Val Gln Val Ala Pro Ala Ala Pro Ala Pro Val Pro Ala Pro
 100 105 110
 Ala Leu Val Pro Val Pro Ala Pro Ala Ala Ala Gln Ala Ser Ala Pro
 115 120 125
 Ala Gln Thr Gln Ala Pro Thr Ser Ala Pro Ala Val Ala Pro Thr
 130 135 140

<210> 5
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:oligonucleotide
 primer for PCR reaction

 <400> 5
 tacggatccg aatcgaacaa aactgcagct g 31

 <210> 6
 <211> 32
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:oligonucleotide
 primer for PCR reaction

 <400> 6
 atactcgagt catggagctg gagttggagc ca 32

 <210> 7
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:oligonucleotide
 primer for PCR reaction

 <400> 7
 gtttgacctg caatccagac aa 22

 <210> 8
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:oligonucleotide
 primer for PCR reaction

 <400> 8
 cccaggatct gaatgggagt t 21

 <210> 9
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:oligonucleotide

primer for PCR reaction

<400> 9
cagatgggcc tgtgttccac tccaa 25

<210> 10
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide
primer for RACE PCR reaction

<400> 10
gctgacagtt gccctgacgc tgct 24

<210> 11
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide
primer for RACE PCR reaction

<400> 11
cggagacggt gctctagctg ctca 24

<210> 12
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide
primer for RACE PCR reaction

<400> 12
tccttccaac tcttgccctca agttccg 27

<210> 13
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:oligonucleotide
primer for RACE PCR reaction

<400> 13
ggtggcagcg gacaggcagg atac 24

<210> 14
<211> 24
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:oligonucleotide
primer for RACE PCR reaction

<400> 14

gaggcggaga gaactaagag aaga

24

<210> 15

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:oligonucleotide
primer for RACE PCR reaction

<400> 15

gagcggagat ggaggagtaa ttca

24

B¹
cont